


```

tgg agg ata gaa aaa gtt ccc aaa gtt tgc cgg ctg caa gtg agt gtg 344
Trp Arg Ile Glu Lys Val Pro Lys Val Cys Arg Leu Gln Val Ser Val
          90                      95                      100

gac gac cag tgt gag ggg tcc aca gaa aag tat ttc ttt aat cta agt 392
Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys Tyr Phe Phe Asn Leu Ser
          105                      110                      115

tcc atg aca tgt gaa aaa ttc ttt tcc ggt ggg tgt cac cgg aac cgg 440
Ser Met Thr Cys Glu Lys Phe Phe Ser Gly Gly Cys His Arg Asn Arg
          120                      125                      130

att gag aac agg ttt cca gat gaa gct act tgt atg ggc ttc tgc gca 488
Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr Cys Met Gly Phe Cys Ala
          135                      140                      145                      150

cca aag aaa att cca tca ttt tgc tac agt cca aaa gat gag gga ctg 536
Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu
          155                      160                      165

tgc tct gcc aat gtg act cgc tat tat ttt aat cca aga tac aga acc 584
Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr
          170                      175                      180

tgt gat gct ttc acc tat act ggc tgt gga ggg aat gac aat aac ttt 632
Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn Asn Phe
          185                      190                      195

gtt agc agg gag gat tgc aaa cgt gca tgt gca aaa gct ttg aaa aag 680
Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys
          200                      205                      210

aaa aag aag atg cca aag ctt cgc ttt gcc agt aga atc cgg aaa att 728
Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile
          215                      220                      225                      230

cgg aag aag caa ttt taa acattcttaa tatgtcatct tgtttgtctt 776
Arg Lys Lys Gln Phe *
          235

tatggccttat ttgcctttat gggtgtatct gaagaataat atgacagcat gaggaacaa 836
atcattggtg atttattcac cagtttttat taatacaagt cactttttca aaaatttgga 896
tttttttata tataactagc tgctattcaa atgtgagctc accattttta atttatggtt 956
caactgtttg tgagactgaa ttc 979

```

<210> 2

<211> 235

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
  1          5          10          15
Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
          20          25          30
Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
          35          40          45
Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
          50          55          60
Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
          65          70          75          80
Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Gln | Val | Ser | Val | Asp | Asp | Gln | Cys | Glu | Gly | Ser | Thr | Glu | Lys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Tyr | Phe | Phe | Asn | Leu | Ser | Ser | Met | Thr | Cys | Glu | Lys | Phe | Phe | Ser | Gly |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gly | Cys | His | Arg | Asn | Arg | Ile | Glu | Asn | Arg | Phe | Pro | Asp | Glu | Ala | Thr |
| | 130 | | | | | 135 | | 1 | | | 140 | | | | |
| Cys | Met | Gly | Phe | Cys | Ala | Pro | Lys | Lys | Ile | Pro | Ser | Phe | Cys | Tyr | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Pro | Lys | Asp | Glu | Gly | Leu | Cys | Ser | Ala | Asn | Val | Thr | Arg | Tyr | Tyr | Phe |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Asn | Pro | Arg | Tyr | Arg | Thr | Cys | Asp | Ala | Phe | Thr | Tyr | Thr | Gly | Cys | Gly |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gly | Asn | Asp | Asn | Asn | Phe | Val | Ser | Arg | Glu | Asp | Cys | Lys | Arg | Ala | Cys |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ala | Lys | Ala | Leu | Lys | Lys | Lys | Lys | Lys | Met | Pro | Lys | Leu | Arg | Phe | Ala |
| | 210 | | | | 215 | | | | | | 220 | | | | |
| Ser | Arg | Ile | Arg | Lys | Ile | Arg | Lys | Lys | Gln | Phe | | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | |

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<210> 3
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>
<223> Oligonucleotide ZC4792

<400> 3
gttgattgctg ttgcctccgc agcctccgta 30

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<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>
<223> Oligonucleotide ZC6281

```
<400> 4
acagatctcc gcgttatttc ctgttggttc 30
```

```
<210> 5
<211> 38
<212> DNA
<213> Artificial Sequence
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<220>
<223> Clone M-2161

<400> 5
gctgagagat tggagaagag agagatctgt ctctgcc 38

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<210> 6
<211> 34
<212> DNA
<213> Artificial Sequence
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<220>
<223> M-2177

<400> 6
 gaaacctcta gacttatatc ctccagcaag catc 34

<210> 7
 <211> 235
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (77)...(235)

<400> 7
 gaattccatt caagaatagt tcaaacaaga agattacaaa ctatcaattt catacacaat 60
 ataaacgacc aaaaga atg aag gct gtt ttc ttg gtt ttg tcc ttg atc gga 112
 Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly
 1 5 10

ttc tgc tgg gcc caa cca gtc act ggc gat gaa tca tct gtt gag att 160
 Phe Cys Trp Ala Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile
 15 20 25

ccg gaa gag tct ctg atc atc gct gaa aac acc act ttg gct aac gtc 208
 Pro Glu Glu Ser Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val
 30 35 40

gcc atg gct gag aga ttg gag aag aga 235
 Ala Met Ala Glu Arg Leu Glu Lys Arg
 45 50

<210> 8
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala
 1 5 10 15
 Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser
 20 25 30
 Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu
 35 40 45
 Arg Leu Glu Lys Arg
 50

<210> 9
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nor-1478

<400> 9
 gtaaaacgac ggccagt 17

<210> 10
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NOR-2523

<400> 10
 tctcttctcc aatctctcag c

21

<210> 11
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> M-2162

<400> 11
 cttttactct agacttactt tggcgcgag aagcc

35

<210> 12
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-terminal

<400> 12
 Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
 1 5 10

<210> 13
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-terminal

<400> 13
 Ala Gln Glu Pro Thr Gly Asn Asn
 1 5

<210> 14
 <211> 165
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> variation
 <222> (0)...(0)
 <223> Kunitz domain

<221> variation
 <222> (1)...(3)
 <223> Codon-1 Wherein the nucleotide triplet 1-3
 encodes any amino acid except cysteine.

<221> variation
 <222> (4)...(6)
 <223> Codon-2 Wherein the nucleotide triplet 4-6

```
<221> variation
<222> (160)...(162)
<223> Codon-54 Wherein the nucleotide triplet 160-162
      encodes any amino acid except cysteine.
```

```
<221> variation
<222> (163)...(165)
<223> Codon-55 Wherein the nucleotide triplet 163-165
        encodes any amino acid except cysteine.
```

```
<400> 14
nnnnnntgtc  tcctgccct  agactacgga  ccctgccggg  ccctacttct  ccgttactac  60
tacgacaggt  acacgcagag  ctgccgccag  ttctgtacg  ggggctgcga  gggcaacgcc  120
aacaatttct  acacctggga  ggcttgcgac  gatgcttgcn  nnnnnn      165
```

```
<210> 15
<211> 55
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Kunitz Domain

```
<221> VARIANT
<222> (1)...(2)
<223> aa1-2  Wherein each amino acid from position 1 to
          2 is individually any amino acid except cysteine.
```

```
<221> VARIANT
<222> (54)...(55)
<223> aa54-55  Wherein each amino acid from position 54
to 55 is individually any amino acid except
cysteine.
```

```

<400> 15
Xaa Xaa Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu
  1      5      10      15
Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu
      20      25      30
Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala
      35      40      45
Cys Asp Asp Ala Cys Xaa Xaa
      50      55

```